

16C/ #7
1653 RECEIVED

NOV 13 2001

OIPE

TECH CENTER 1600/2900

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/697,089

DATE: 06/29/2001

TIME: 14:09:54

Input Set : A:\07334-136001.TXT

Output Set: N:\CRF3\06292001\I697089.raw

ENTERED

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4 <110> APPLICANT: Bertin, John
5      Robison, Keith E.
7 <120> TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
8      PROTEIN FAMILY AND USES THEREOF
11 <130> FILE REFERENCE: 07334-136001
13 <140> CURRENT APPLICATION NUMBER: US 09/697,089
14 <141> CURRENT FILING DATE: 2000-10-26
16 <150> PRIOR APPLICATION NUMBER: US 60/161,822
17 <151> PRIOR FILING DATE: 1999-10-27
19 <160> NUMBER OF SEQ ID NOS: 12
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 3133
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (36)...(3107)
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34                                     Met Asn Phe Ile Lys Asp
35                                     1           5
37 aat agc cga gcc ctt att caa aga atg gga atg act gtt ata aag caa      101
38 Asn Ser Arg Ala Leu Ile Gln Arg Met Gly Met Thr Val Ile Lys Gln
39           10           15           20
41 atc aca gat gac cta ttt gta tgg aat gtt ctg aat cgc gaa gaa gta      149
42 Ile Thr Asp Asp Leu Phe Val Trp Asn Val Leu Asn Arg Glu Glu Val
43           25           30           35
45 aac atc att tgc tgc gag aag gtg gag cag gat gct gct aga ggg atc      197
46 Asn Ile Ile Cys Cys Glu Lys Val Glu Gln Asp Ala Ala Arg Gly Ile
47           40           45           50
49 att cac atg att ttg aaa aag ggt tca gag tcc tgt aac ctc ttt ctt      245
50 Ile His Met Ile Leu Lys Lys Gly Ser Glu Ser Cys Asn Leu Phe Leu
51 55           60           65           70
53 aaa tcc ctt aag gag tgg aac tat cct cta ttt cag gac ttg aat gga      293
54 Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu Phe Gln Asp Leu Asn Gly
55           75           80           85
57 caa agt ctt ttt cat cag aca tca gaa gga gac ttg gac gat ttg gct      341
58 Gln Ser Leu Phe His Gln Thr Ser Glu Gly Asp Leu Asp Asp Leu Ala
59           90           95           100
61 cag gat tta aag gac ttg tac cat acc cca tct ttt ctg aac ttt tat      389
62 Gln Asp Leu Lys Asp Leu Tyr His Thr Pro Ser Phe Leu Asn Phe Tyr
63           105           110           115
65 ccc ctt ggt gaa gat att gac att att ttt aac ttg aaa agc acc ttc      437
66 Pro Leu Gly Glu Asp Ile Asp Ile Ile Phe Asn Leu Lys Ser Thr Phe
67           120           125           130
69 aca gaa cct gtc ctg tgg agg aag gac caa cac cat cac cgc gtg gag      485

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70 Thr Glu Pro Val Leu Trp Arg Lys Asp Gln His His His Arg Val Glu
71 135 140 145 150
73 cag ctg acc ctg aat ggc ctc ctg cag gct ctt cag agc ccc tgc atc 533
74 Gln Leu Thr Leu Asn Gly Leu Leu Gln Ala Leu Gln Ser Pro Cys Ile
75 155 160 165
77 att gaa ggg gaa tct ggc aaa ggc aag tcc act ctg ctg cag cgc att 581
78 Ile Glu Gly Glu Ser Gly Lys Gly Lys Ser Thr Leu Leu Gln Arg Ile
79 170 175 180
81 gcc atg ctc tgg ggc tcc gga aag tgc aag gct ctg acc aag ttc aaa 629
82 Ala Met Leu Trp Gly Ser Gly Lys Cys Lys Ala Leu Thr Lys Phe Lys
83 185 190 195
85 ttc gtc ttc ttc ctc cgt ctc agc agg gcc cag ggt gga ctt ttt gaa 677
86 Phe Val Phe Phe Leu Arg Leu Ser Arg Ala Gln Gly Gly Leu Phe Glu
87 200 205 210
89 acc ctc tgt gat caa ctc ctg gat ata cct ggc aca atc agg aag cag 725
90 Thr Leu Cys Asp Gln Leu Leu Asp Ile Pro Gly Thr Ile Arg Lys Gln
91 215 220 225 230
93 aca ttc atg gcc atg ctg ctg aag ctg cgg cag agg gtt ctt ttc ctt 773
94 Thr Phe Met Ala Met Leu Leu Lys Leu Arg Gln Arg Val Leu Phe Leu
95 235 240 245
97 ctt gat ggc tac aat gaa ttc aag ccc cag aac tgc cca gaa atc gaa 821
98 Leu Asp Gly Tyr Asn Glu Phe Lys Pro Gln Asn Cys Pro Glu Ile Glu
99 250 255 260
101 gcc ctg ata aag gaa aac cac cgc ttc aag aac atg gtc atc gtc acc 869
102 Ala Leu Ile Lys Glu Asn His Arg Phe Lys Asn Met Val Ile Val Thr
103 265 270 275
105 act acc act gag tgc ctg agg cac ata cgg cag ttt ggt gcc ctg act 917
106 Thr Thr Thr Glu Cys Leu Arg His Ile Arg Gln Phe Gly Ala Leu Thr
107 280 285 290
109 gct gag gtg ggg gat atg aca gaa gac agc gcc cag gct ctc atc cga 965
110 Ala Glu Val Gly Asp Met Thr Glu Asp Ser Ala Gln Ala Leu Ile Arg
111 295 300 305 310
113 gaa gtg ctg atc aag gag ctt gct gaa ggc ttg ttg ctc caa att cag 1013
114 Glu Val Leu Ile Lys Glu Leu Ala Glu Gly Leu Leu Leu Gln Ile Gln
115 315 320 325
117 aaa tcc agg tgc ttg agg aat ctc atg aag acc cct ctc ttt gtg gtc 1061
118 Lys Ser Arg Cys Leu Arg Asn Leu Met Lys Thr Pro Leu Phe Val Val
119 330 335 340
121 atc act tgt gca atc cag atg ggt gaa agt gag ttc cac tct cac aca 1109
122 Ile Thr Cys Ala Ile Gln Met Gly Glu Ser Glu Phe His Ser His Thr
123 345 350 355
125 caa aca acg ctg ttc cat acc ttc tat gat ctg ttg ata cag aaa aac 1157
126 Gln Thr Thr Leu Phe His Thr Phe Tyr Asp Leu Leu Ile Gln Lys Asn
127 360 365 370
129 aaa cac aaa cat aaa ggt gtg gct gca agt gac ttc att cgg agc ctg 1205
130 Lys His Lys His Lys Gly Val Ala Ala Ser Asp Phe Ile Arg Ser Leu
131 375 380 385 390
133 gac cac tgt gga gac cta gct ctg gag ggt gtg ttc tcc cac aag ttt 1253
134 Asp His Cys Gly Asp Leu Ala Leu Glu Gly Val Phe Ser His Lys Phe

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135		395		400		405		
137	gat ttc gaa ctg cag gat gtg tcc agc gtg aat gag gat gtc ctg ctg							1301
138	Asp Phe Glu Leu Gln Asp Val Ser Ser Val Asn Glu Asp Val Leu Leu							
139		410		415		420		
141	aca act ggg ctc ctc tgt aaa tat aca got caa agg ttc aag cca aag							1349
142	Thr Thr Gly Leu Leu Cys Lys Tyr Thr Ala Gln Arg Phe Lys Pro Lys							
143		425		430		435		
145	tat aaa ttc ttt cac aag tca ttc cag gag tac aca gca gga cga aga							1397
146	Tyr Lys Phe Phe His Lys Ser Phe Gln Glu Tyr Thr Ala Gly Arg Arg							
147		440		445		450		
149	ctc agc agt tta ttg acg tct cat gag cca gag gag gtg acc aag ggg							1445
150	Leu Ser Ser Leu Leu Thr Ser His Glu Pro Glu Glu Val Thr Lys Gly							
151	455		460		465		470	
153	aat ggt tac ttg cag aaa atg gtt tcc att tcg gac att aca tcc act							1493
154	Asn Gly Tyr Leu Gln Lys Met Val Ser Ile Ser Asp Ile Thr Ser Thr							
155		475		480		485		
157	tat agc agc ctg ctc cgg tac acc tgt ggg tca tct gtg gaa gcc acc							1541
158	Tyr Ser Ser Leu Leu Arg Tyr Thr Cys Gly Ser Ser Val Glu Ala Thr							
159		490		495		500		
161	agg gct gtt atg aag cac ctc gca gca gtg tat caa cac ggc tgc ctt							1589
162	Arg Ala Val Met Lys His Leu Ala Ala Val Tyr Gln His Gly Cys Leu							
163		505		510		515		
165	ctc gga ctt tcc atc gcc aag agg cct ctc tgg aga cag gaa tct ttg							1637
166	Leu Gly Leu Ser Ile Ala Lys Arg Pro Leu Trp Arg Gln Glu Ser Leu							
167		520		525		530		
169	caa agt gtg aaa aac acc act gag caa gaa att ctg aaa gcc ata aac							1685
170	Gln Ser Val Lys Asn Thr Thr Glu Gln Glu Ile Leu Lys Ala Ile Asn							
171	535		540		545		550	
173	atc aat tcc ttt gta gag tgt ggc atc cat tta tat caa gag agt aca							1733
174	Ile Asn Ser Phe Val Glu Cys Gly Ile His Leu Tyr Gln Glu Ser Thr							
175		555		560		565		
177	tcc aaa tca gcc ctg agc caa gaa ttt gaa gct ttc ttt caa ggt aaa							1781
178	Ser Lys Ser Ala Leu Ser Gln Glu Phe Glu Ala Phe Phe Gln Gly Lys							
179		570		575		580		
181	agc tta tat atc aac tca ggg aac atc ccc gat tac tta ttt gac ttc							1829
182	Ser Leu Tyr Ile Asn Ser Gly Asn Ile Pro Asp Tyr Leu Phe Asp Phe							
183		585		590		595		
185	ttt gaa cat ttg ccc aat tgt gca agt gct ctg gac ttc att aaa ctg							1877
186	Phe Glu His Leu Pro Asn Cys Ala Ser Ala Leu Asp Phe Ile Lys Leu							
187		600		605		610		
189	gac ttt tat ggg gga gct atg gct tca tgg gaa aag gct gca gaa gac							1925
190	Asp Phe Tyr Gly Gly Ala Met Ala Ser Trp Glu Lys Ala Ala Glu Asp							
191	615		620		625		630	
193	aca ggt gga atc cac atg gaa gag gcc cca gaa acc tac att ccc agc							1973
194	Thr Gly Gly Ile His Met Glu Glu Ala Pro Glu Thr Tyr Ile Pro Ser							
195		635		640		645		
197	agg gct gta tct ttg ttc ttc aac tgg aag cag gaa ttc agg act ctg							2021
198	Arg Ala Val Ser Leu Phe Phe Asn Trp Lys Gln Glu Phe Arg Thr Leu							
199		650		655		660		

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201	gag	gtc	aca	ctc	cgg	gat	ttc	agc	aag	ttg	aat	aag	caa	gat	atc	aca	2069
202	Glu	Val	Thr	Leu	Arg	Asp	Phe	Ser	Lys	Leu	Asn	Lys	Gln	Asp	Ile	Thr	
203			665					670					675				
205	tat	ctg	ggg	aaa	ata	ttc	agc	tct	gcc	aca	agc	ctc	agg	ctg	caa	ata	2117
206	Tyr	Leu	Gly	Lys	Ile	Phe	Ser	Ser	Ala	Thr	Ser	Leu	Arg	Leu	Gln	Ile	
207			680				685					690					
209	aag	aga	tgt	gct	ggt	gtg	gct	gga	agc	ctc	agt	ttg	gtc	ctc	agc	acc	2165
210	Lys	Arg	Cys	Ala	Gly	Val	Ala	Gly	Ser	Leu	Ser	Leu	Val	Leu	Ser	Thr	
211	695						700				705					710	
213	tgt	aag	aac	att	tat	tct	ctc	atg	gtg	gaa	gcc	agt	ccc	ctc	acc	ata	2213
214	Cys	Lys	Asn	Ile	Tyr	Ser	Leu	Met	Val	Glu	Ala	Ser	Pro	Leu	Thr	Ile	
215					715					720					725		
217	gaa	gat	gag	agg	cac	atc	aca	tct	gta	aca	aac	ctg	aaa	acc	ttg	agt	2261
218	Glu	Asp	Glu	Arg	His	Ile	Thr	Ser	Val	Thr	Asn	Leu	Lys	Thr	Leu	Ser	
219				730						735				740			
221	att	cat	gac	cta	cag	aat	caa	cgg	ctg	ccg	ggt	ggt	ctg	act	gac	agc	2309
222	Ile	His	Asp	Leu	Gln	Asn	Gln	Arg	Leu	Pro	Gly	Gly	Leu	Thr	Asp	Ser	
223			745					750					755				
225	ttg	ggt	aac	ttg	aag	aac	ctt	aca	aag	ctc	ata	atg	gat	aac	ata	aag	2357
226	Leu	Gly	Asn	Leu	Lys	Asn	Leu	Thr	Lys	Leu	Ile	Met	Asp	Asn	Ile	Lys	
227		760					765					770					
229	atg	aat	gaa	gaa	gat	gct	ata	aaa	cta	gct	gaa	ggc	ctg	aaa	aac	ctg	2405
230	Met	Asn	Glu	Glu	Asp	Ala	Ile	Lys	Leu	Ala	Glu	Gly	Leu	Lys	Asn	Leu	
231	775					780				785						790	
233	aag	aag	atg	tgt	tta	ttt	cat	ttg	acc	cac	ttg	tct	gac	att	gga	gag	2453
234	Lys	Lys	Met	Cys	Leu	Phe	His	Leu	Thr	His	Leu	Ser	Asp	Ile	Gly	Glu	
235						795				800						805	
237	gga	atg	gat	tac	ata	gtc	aag	tct	ctg	tca	agt	gaa	ccc	tgt	gac	ctt	2501
238	Gly	Met	Asp	Tyr	Ile	Val	Lys	Ser	Leu	Ser	Ser	Glu	Pro	Cys	Asp	Leu	
239				810					815					820			
241	gaa	gaa	att	caa	tta	gtc	tcc	tgc	tgc	ttg	tct	gca	aat	gca	gtg	aaa	2549
242	Glu	Glu	Ile	Gln	Leu	Val	Ser	Cys	Cys	Leu	Ser	Ala	Asn	Ala	Val	Lys	
243			825					830					835				
245	atc	cta	gct	cag	aat	ctt	cac	aat	ttg	gtc	aaa	ctg	agc	att	ctt	gat	2597
246	Ile	Leu	Ala	Gln	Asn	Leu	His	Asn	Leu	Val	Lys	Leu	Ser	Ile	Leu	Asp	
247		840					845					850					
249	tta	tca	gaa	aat	tac	ctg	gaa	aaa	gat	gga	aat	gaa	gct	ctt	cat	gaa	2645
250	Leu	Ser	Glu	Asn	Tyr	Leu	Glu	Lys	Asp	Gly	Asn	Glu	Ala	Leu	His	Glu	
251	855					860					865					870	
253	ctg	atc	gac	agg	atg	aac	gtg	cta	gaa	cag	ctc	acc	gca	ctg	atg	ctg	2693
254	Leu	Ile	Asp	Arg	Met	Asn	Val	Leu	Glu	Gln	Leu	Thr	Ala	Leu	Met	Leu	
255						875				880						885	
257	ccc	tgg	ggc	tgt	gac	gtg	caa	ggc	agc	ctg	agc	agc	ctg	ttg	aaa	cat	2741
258	Pro	Trp	Gly	Cys	Asp	Val	Gln	Gly	Ser	Leu	Ser	Ser	Leu	Leu	Lys	His	
259						890				895					900		
261	ttg	gag	gag	gtc	cca	caa	ctc	gtc	aag	ctt	ggg	ttg	aaa	aac	tgg	aga	2789
262	Leu	Glu	Glu	Val	Pro	Gln	Leu	Val	Lys	Leu	Gly	Leu	Lys	Asn	Trp	Arg	
263			905					910					915				
265	ctc	aca	gat	aca	gag	att	aga	att	tta	ggt	gca	ttt	ttt	gga	aag	aac	2837

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266 Leu Thr Asp Thr Glu Ile Arg Ile Leu Gly Ala Phe Phe Gly Lys Asn
267      920                      925                      930
269 cct ctg aaa aac ttc cag cag ttg aat ttg gcg gga aat cgt gtg agc      2885
270 Pro Leu Lys Asn Phe Gln Gln Leu Asn Leu Ala Gly Asn Arg Val Ser
271 935                      940                      945                      950
273 agt gat gga tgg ctt gcc ttc atg ggt gta ttt gag aat ctt aag caa      2933
274 Ser Asp Gly Trp Leu Ala Phe Met Gly Val Phe Glu Asn Leu Lys Gln
275                      955                      960                      965
277 tta gtg ttt ttt gac ttt agt act aaa gaa ttt cta cct gat cca gca      2981
278 Leu Val Phe Phe Asp Phe Ser Thr Lys Glu Phe Leu Pro Asp Pro Ala
279                      970                      975                      980
281 tta gtc aga aaa ctt agc caa gtg tta tcc aag tta act ttt ctg caa      3029
282 Leu Val Arg Lys Leu Ser Gln Val Leu Ser Lys Leu Thr Phe Leu Gln
283                      985                      990                      995
285 gaa gct agg ctt gtt ggg tgg caa ttt gat gat gat gat ctc agt gtt      3077
286 Glu Ala Arg Leu Val Gly Trp Gln Phe Asp Asp Asp Asp Leu Ser Val
287      1000                      1005                      1010
289 att aca ggt gct ttt aaa cta gta act gct taaataaagt gtactcgaag      3127
290 Ile Thr Gly Ala Phe Lys Leu Val Thr Ala
291 1015                      1020
293 ccagta      3133
295 <210> SEQ ID NO: 2
296 <211> LENGTH: 1024
297 <212> TYPE: PRT
298 <213> ORGANISM: Homo sapiens
300 <400> SEQUENCE: 2
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303 Met Thr Val Ile Lys Gln Ile Thr Asp Asp Leu Phe Val Trp Asn Val
304      20      25      30
305 Leu Asn Arg Glu Glu Val Asn Ile Cys Cys Glu Lys Val Glu Gln
306      35      40      45
307 Asp Ala Ala Arg Gly Ile Ile His Met Ile Leu Lys Lys Gly Ser Glu
308      50      55      60
309 Ser Cys Asn Leu Phe Leu Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu
310 65      70      75      80
311 Phe Gln Asp Leu Asn Gly Gln Ser Leu Phe His Gln Thr Ser Glu Gly
312      85      90      95
313 Asp Leu Asp Asp Leu Ala Gln Asp Leu Lys Asp Leu Tyr His Thr Pro
314      100      105      110
315 Ser Phe Leu Asn Phe Tyr Pro Leu Gly Glu Asp Ile Asp Ile Ile Phe
316      115      120      125
317 Asn Leu Lys Ser Thr Phe Thr Glu Pro Val Leu Trp Arg Lys Asp Gln
318      130      135      140
319 His His His Arg Val Glu Gln Leu Thr Leu Asn Gly Leu Leu Gln Ala
320 145      150      155      160
321 Leu Gln Ser Pro Cys Ile Ile Glu Gly Glu Ser Gly Lys Gly Lys Ser
322      165      170      175
323 Thr Leu Leu Gln Arg Ile Ala Met Leu Trp Gly Ser Gly Lys Cys Lys

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